

SEQUENCE LISTING

<110> Matuschek, Markus
Heinekamp, Thorsten
Schmidt, Andre
Brakhage, Axel

<120> Method for the genetic modification of organisms of the genus
Blakeslea, corresponding organisms, and the use of the same

<130> 13311-00010-US

<150> PCT/EP2004/000100

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<150> DE 103 00 649.4

<151> 2003-01-09

<150> DE 103 41 272.7

<151> 2003-09-08

<160> 80

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 Met Gln Leu Ala
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 Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala Glu Ala Leu Lys
 5 10 15 20
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 Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val Leu Arg Thr Trp
 25 30 35
 gcg acc cag tac tcg ctt ccg tca gaa gag tca gac gcg gcc cgc ccg 321
 Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp Ala Ala Arg Pro
 40 45 50
 gga ctg aag aat gcc tac aag cca cca cct tcc gac aca aag ggc atc 369
 Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp Thr Lys Gly Ile
 55 60 65
 aca atg gcg cta cgt gtc atc ggc tcc tgg gcc gca gtg ttc ctc cac 417
 Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala Val Phe Leu His
 70 75 80
 gcc att ttt caa atc aag ctt ccg acc tcc ttg gac cag ctg cac tgg 465
 Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp Gln Leu His Trp
 85 90 95 100
 ctg ccc gtg tca gat gcc aca gct cag ctg gtt agc ggc acg agc agc 513
 Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser Gly Thr Ser Ser
 105 110 115

ctg ctc gac atc gtc gta gta ttc ttt gtc ctg gag ttc ctg tac aca Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu Phe Leu Tyr Thr	561
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ggc ctt ttt atc acc acg cat gat gct atg cat ggc acc atc gcc atg Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly Thr Ile Ala Met	609
135 140 145	
aga aac agg cag ctt aat gac ttc ttg ggc aga gta tgc atc tcc ttg Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val Cys Ile Ser Leu	657
150 155 160	
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165 170 175 180	
cac aac cac act ggc gag gtg ggc aag gac cct gac ttc cac agg gga His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Arg Gly	753
185 190 195	
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200 205 210	
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230 235 240	
ccc atc ctg tcc gcc ttc cgc ttg ttc tac ttt ggc acg tac atg ccc Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Met Pro	945
245 250 255 260	
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aac tgg tgg aag tcg cgc act agc cag gcg tcc gac ctg gtc agc ttt Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp Leu Val Ser Phe	1041
280 285 290	
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295 300 305	
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310 315 320	
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 <212> PRT
 <213> Haematococcus pluvialis

<400> 12

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 35 40 45

Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
 50 55 60

Thr Lys Gly Ile Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala
 65 70 75 80

Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
 85 90 95

Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
 100 105 110

Gly Thr Ser Ser Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu
 115 120 125

Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
 130 135 140

Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
 145 150 155 160

Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
 165 170 175

His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
 180 185 190

Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
 195 200 205

Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
 210 215 220

Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
 225 230 235 240

Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
 245 250 255

Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
 260 265 270

Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
 275 280 285

Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
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ctccgtcctc tgccaaatct cgcgtcgggg cctgcctaag tcgaaga atg cac gtc      176
                               Met His Val
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gca tcg gca cta atg gtc gag cag aaa ggc agt gag gca gct gct tcc      224
Ala Ser Ala Leu Met Val Glu Gln Lys Gly Ser Glu Ala Ala Ala Ser
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agc cca gac gtc ttg aga gcg tgg gcg aca cag tat cac atg cca tcc      272
Ser Pro Asp Val Leu Arg Ala Trp Ala Thr Gln Tyr His Met Pro Ser
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gag tcg tca gac gca gct cgt cct gcg cta aag cac gcc tac aaa cct      320
Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala Tyr Lys Pro
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cca gca tct gac gcc aag ggc atc acg atg gcg ctg acc atc att ggc      368
Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr Ile Ile Gly
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acc tgg acc gca gtg ttt tta cac gca ata ttt caa atc agg cta ccg      416
Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile Arg Leu Pro
      70                               75                               80

aca tcc atg gac cag ctt cac tgg ttg cct gtg tcc gaa gcc aca gcc      464
Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu Ala Thr Ala
      85                               90                               95

cag ctt ttg ggc gga agc agc agc cta ctg cac atc gct gca gtc ttc      512
Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala Ala Val Phe
      100                               105                               110                               115

att gta ctt gag ttc ctg tac act ggt cta ttc atc acc aca cat gac      560
Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp
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gca atg cat ggc acc ata gct ttg agg cac agg cag ctc aat gat ctc      608
Ala Met His Gly Thr Ile Ala Leu Arg His Arg Gln Leu Asn Asp Leu
                               135                               140                               145

ctt ggc aac atc tgc ata tca ctg tac gcc tgg ttt gac tac agc atg      656
Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Ser Met
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 35 40 45

Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr
 50 55 60

Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile
 65 70 75 80

Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu
 85 90 95

Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala
 100 105 110

Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr
 115 120 125

Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg His Arg Gln Leu
 130 135 140

Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp
 145 150 155 160

Tyr Ser Met Leu His Arg Lys His Trp Glu His His Asn His Thr Gly
 165 170 175

Glu Val Gly Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val
 180 185 190

Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe

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Phe Arg Leu Phe Tyr	Phe Gly Thr Tyr	Leu Pro His Lys Pro Glu Pro
245	250	255
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260	265	270
Ser Glu Ala Ser Asp Val	Met Ser Phe Leu Thr Cys	Tyr His Phe Asp
275	280	285
Leu His Trp Glu His His	Arg Trp Pro Phe Ala	Pro Trp Trp Gln Leu
290	295	300
Pro His Cys Arg Arg	Leu Ser Gly Arg Gly	Leu Val Pro Ala Leu Ala
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Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His	
20 25 30	
gcg ctg tgg ttt ctg gac gca gcg gcg cat ccc atc ctg gcg atc gca	144
Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala	
35 40 45	
aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg	192
Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala	
50 55 60	

cat gac gcg atg cac ggg tcg gtg gtg ccg ggg cgt ccg cgc gcc aat 240
His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
65 70 75 80

gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg 288
Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
85 90 95

cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc 336
 Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
 100 105 110

gac gac gac ccc gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc 384
Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
115 120 125

cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc 432
Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
130 135 140

gtc atc gtg acg gtc tat gcg ctg atc ctt ggg gat cgc tgg atg tac 480
Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145 150 155 160

gtg gtc ttc tgg ccg ctg ccg tcg atc ctg gcg tcg atc cag ctg ttc 528
Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
165 170 175

gtg ttc ggc acc tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg 576
Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
180 185 190

gac cgc cac aat gcg cgg tcg tcg cgg atc agc gac ccc gtg tcg ctg 624
Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
195 200 205

ctg acc tgc ttt cac ttt ggc ggt tat cat cac gaa cac cac ctg cac 672
Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
210 215 220

cgc acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac 720
Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
225 230 235 240

acc gca tga	729
Thr Ala	

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<210> 16
<211> 242
<212> PRT
<213> Agrobacterium aurantiacum
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<400> 16

Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
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Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
20 25 30

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala
35 40 45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
65 70 75 80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
85 90 95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
130 135 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
180 185 190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
210 215 220

Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp

225

230

235

240

Thr Ala

<210> 17

<211> 1631

<212> DNA

<213> *Alcaligenes* sp.

<220>

<221> CDS

<222> (99) .. (827)

<400> 17

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 Met Ser Gly Arg Lys Pro
 1 5

ggc aca act ggc gac acg atc gtc aat ctc ggt ctg acc gcc gcg atc 164
 Gly Thr Thr Gly Asp Thr Ile Val Asn Leu Gly Leu Thr Ala Ala Ile
 10 15 20

ctg ctg tgc tgg ctg gtc ctg cac gcc ttt acg cta tgg ttg cta gat 212
 Leu Leu Cys Trp Leu Val Leu His Ala Phe Thr Leu Trp Leu Leu Asp
 25 30 35

gcg gcc gcg cat ccg ctg ctt gcc gtg ctg tgc ctg gct ggg ctg acc 260
 Ala Ala Ala His Pro Leu Leu Ala Val Leu Cys Leu Ala Gly Leu Thr
 40 45 50

tgg ctg tgc gtc ggg ctg ttc atc atc gcg cat gac gca atg cac ggg 308
 Trp Leu Ser Val Gly Leu Phe Ile Ile Ala His Asp Ala Met His Gly
 55 60 65 70

tcc gtg gtg ccg ggg cgg ccg cgc gcc aat gcg gcg atc ggg caa ctg 356
 Ser Val Val Pro Gly Arg Pro Arg Ala Asn Ala Ala Ile Gly Gln Leu
 75 80 85

gcg ctg tgg ctc tat gcg ggg ttc tcg tgg ccc aag ctg atc gcc aag 404
 Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp Pro Lys Leu Ile Ala Lys
 90 95 100

cac atg acg cat cac cgg cac gcc ggc acc gac aac gat ccc gat ttc 452
 His Met Thr His His Arg His Ala Gly Thr Asp Asn Asp Pro Asp Phe
 105 110 115

ggt cac gga ggg ccc gtg cgc tgg tac gcc agc ttc gtc tcc acc tat 500
 Gly His Gly Gly Pro Val Arg Trp Tyr Gly Ser Phe Val Ser Thr Tyr
 120 125 130

ttc ggc tgg cga gag gga ctg ctg cta ccg gtg atc gtc acc acc tat 548

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<211> 242
 <212> PRT
 <213> Alcaligenes sp.

<400> 18

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Gly Leu Thr Ala Ala Ile Leu Leu Cys Trp Leu Val Leu His Ala Phe
 20 25 30

Thr Leu Trp Leu Leu Asp Ala Ala Ala His Pro Leu Leu Ala Val Leu
 35 40 45

Cys Leu Ala Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

Ala Ala Ile Gly Gln Leu Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95

Pro Lys Leu Ile Ala Lys His Met Thr His His Arg His Ala Gly Thr
 100 105 110

Asp Asn Asp Pro Asp Phe Gly His Gly Gly Pro Val Arg Trp Tyr Gly
 115 120 125

Ser Phe Val Ser Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
 130 135 140

Val Ile Val Thr Thr Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
 145 150 155 160

Val Ile Phe Trp Pro Val Pro Ala Val Leu Ala Ser Ile Gln Ile Phe
 165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Asp Phe Pro
 180 185 190

Asp Arg His Asn Ala Arg Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu
 195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
 210 215 220

Pro His Val Pro Trp Trp Arg Leu Pro Arg Thr Arg Lys Thr Gly Gly
 225 230 235 240

Arg Ala

<210> 19
 <211> 729
 <212> DNA
 <213> *Paracoccus marcusii*

<220>
 <221> CDS
 <222> (1)..(729)

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 Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
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 Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
 20 25 30

gcg ctg tgg ttt ctg gac gcg gcg gcc cat ccc atc ctg gcg gtc gcg 144
 Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Val Ala
 35 40 45

aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg 192
 Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

cat gac gcg atg cac ggg tcg gtc gtg ccg ggg cgt ccg cgc gcc aat 240
 His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg 288
 Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95

cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc 336
 Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
 100 105 110

gac gac gac cca gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc 384
 Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
 115 120 125

cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc 432

Arg	Phe	Ile	Gly	Thr	Tyr	Phe	Gly	Trp	Arg	Glu	Gly	Leu	Leu	Leu	Pro		
130						135					140						
gtc	atc	gtg	acg	gtc	tat	gcg	ctg	atc	ctg	ggg	gat	cgc	tgg	atg	tac	480	
Val	Ile	Val	Thr	Val	Tyr	Ala	Leu	Ile	Leu	Gly	Asp	Arg	Trp	Met	Tyr		
145					150					155					160		
gtg	gtc	ttc	tgg	ccg	ttg	ccg	tcg	atc	ctg	gcg	tcg	atc	cag	ctg	ttc	528	
Val	Val	Phe	Trp	Pro	Leu	Pro	Ser	Ile	Leu	Ala	Ser	Ile	Gln	Leu	Phe		
				165					170					175			
gtg	ttc	ggc	act	tgg	ctg	ccg	cac	cgc	ccc	ggc	cac	gac	gcg	ttc	ccg	576	
Val	Phe	Gly	Thr	Trp	Leu	Pro	His	Arg	Pro	Gly	His	Asp	Ala	Phe	Pro		
			180					185					190				
gac	cgc	cat	aat	gcg	cgg	tcg	tcg	cgg	atc	agc	gac	cct	gtg	tcg	ctg	624	
Asp	Arg	His	Asn	Ala	Arg	Ser	Ser	Arg	Ile	Ser	Asp	Pro	Val	Ser	Leu		
		195				200						205					
ctg	acc	tgc	ttt	cat	ttt	ggc	ggt	tat	cat	cac	gaa	cac	cac	ctg	cac	672	
Leu	Thr	Cys	Phe	His	Phe	Gly	Gly	Tyr	His	His	Glu	His	His	Leu	His		
	210					215					220						
ccg	acg	gtg	ccg	tgg	tgg	cgc	ctg	ccc	agc	acc	cgc	acc	aag	ggg	gac	720	
Pro	Thr	Val	Pro	Trp	Trp	Arg	Leu	Pro	Ser	Thr	Arg	Thr	Lys	Gly	Asp		
225				230					235					240			
acc	gca	tga														729	
Thr	Ala																
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<212>	PRT																
<213>	Paracoccus marcusii																
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Met	Ser	Ala	His	Ala	Leu	Pro	Lys	Ala	Asp	Leu	Thr	Ala	Thr	Ser	Leu		
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Ile	Val	Ser	Gly	Gly	Ile	Ile	Ala	Ala	Trp	Leu	Ala	Leu	His	Val	His		
			20				25						30				
Ala	Leu	Trp	Phe	Leu	Asp	Ala	Ala	Ala	His	Pro	Ile	Leu	Ala	Val	Ala		
		35				40						45					
Asn	Phe	Leu	Gly	Leu	Thr	Trp	Leu	Ser	Val	Gly	Leu	Phe	Ile	Ile	Ala		
	50					55					60						
His	Asp	Ala	Met	His	Gly	Ser	Val	Val	Pro	Gly	Arg	Pro	Arg	Ala	Asn		
65					70					75					80		

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
 100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
 115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
 130 135 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
 145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
 165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
 180 185 190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
 195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
 210 215 220

Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
 225 230 235 240

Thr Ala

<210> 21
 <211> 1629
 <212> DNA
 <213> Synechocystis sp.

<220>
 <221> CDS
 <222> (1)..(1629)

<400> 21

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gtc tgt gca gcc tat ttg ctc caa cgg ggc ttg ggg gtg acg tta cta	96
Val Cys Ala Ala Tyr Leu Leu Gln Arg Gly Leu Gly Val Thr Leu Leu	
20 25 30	
gaa aag cgg gaa gta cca ggg ggg gcg gcc acc aca gaa gct ctc atg	144
Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met	
35 40 45	
ccg gag cta tcc ccc cag ttt cgc ttt aac cgc tgt gcc att gac cac	192
Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His	
50 55 60	
gaa ttt atc ttt ctg ggg ccg gtg ttg cag gag cta aat tta gcc cag	240
Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln	
65 70 75 80	
tat ggt ttg gaa tat tta ttt tgt gac ccc agt gtt ttt tgt ccg ggg	288
Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly	
85 90 95	
ctg gat ggc caa gct ttt atg agc tac cgt tcc cta gaa aaa acc tgt	336
Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys	
100 105 110	
gcc cac att gcc acc tat agc ccc cga gat gcg gaa aaa tat cgg caa	384
Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln	
115 120 125	
ttt gtc aat tat tgg acg gat ttg ctc aac gct gtc cag cct gct ttt	432
Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe	
130 135 140	
aat gct ccg ccc cag gct tta cta gat tta gcc ctg aac tat ggt tgg	480
Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp	
145 150 155 160	
gaa aac tta aaa tcc gtg ctg gcg atc gcc ggg tcg aaa acc aag gcg	528
Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala	
165 170 175	
ttg gat ttt atc cgc act atg atc ggc tcc ccg gaa gat gtg ctc aat	576
Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn	
180 185 190	
gaa tgg ttc gac agc gaa cgg gtt aaa gct cct tta gct aga cta tgt	624
Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys	
195 200 205	
tcg gaa att ggc gct ccc cca tcc caa aag ggt agt agc tcc ggc atg	672
Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met	
210 215 220	
atg atg gtg gcc atg cgg cat ttg gag gga att gcc aga cca aaa gga	720

Met	Met	Val	Ala	Met	Arg	His	Leu	Glu	Gly	Ile	Ala	Arg	Pro	Lys	Gly	
225					230					235					240	
ggc	act	gga	gcc	ctc	aca	gaa	gcc	ttg	gtg	aag	tta	gtg	caa	gcc	caa	768
Gly	Thr	Gly	Ala	Leu	Thr	Glu	Ala	Leu	Val	Lys	Leu	Val	Gln	Ala	Gln	
				245					250					255		
ggg	gga	aaa	atc	ctc	act	gac	caa	acc	gtc	aaa	cgg	gta	ttg	gtg	gaa	816
Gly	Gly	Lys	Ile	Leu	Thr	Asp	Gln	Thr	Val	Lys	Arg	Val	Leu	Val	Glu	
			260					265					270			
aac	aac	cag	gcg	atc	ggg	gtg	gag	gta	gct	aac	gga	gaa	cag	tac	cgg	864
Asn	Asn	Gln	Ala	Ile	Gly	Val	Glu	Val	Ala	Asn	Gly	Glu	Gln	Tyr	Arg	
		275					280					285				
gcc	aaa	aaa	ggc	gtg	att	tct	aac	atc	gat	gcc	cgc	cgt	tta	ttt	ttg	912
Ala	Lys	Lys	Gly	Val	Ile	Ser	Asn	Ile	Asp	Ala	Arg	Arg	Leu	Phe	Leu	
	290					295					300					
caa	ttg	gtg	gaa	ccg	ggg	gcc	cta	gcc	aag	gtg	aat	caa	aac	cta	ggg	960
Gln	Leu	Val	Glu	Pro	Gly	Ala	Leu	Ala	Lys	Val	Asn	Gln	Asn	Leu	Gly	
305					310					315					320	
gaa	cga	ctg	gaa	cgg	cgc	act	gtg	aac	aat	aac	gaa	gcc	att	tta	aaa	1008
Glu	Arg	Leu	Glu	Arg	Arg	Thr	Val	Asn	Asn	Asn	Glu	Ala	Ile	Leu	Lys	
				325					330					335		
atc	gat	tgt	gcc	ctc	tcc	ggg	tta	ccc	cac	ttc	act	gcc	atg	gcc	ggg	1056
Ile	Asp	Cys	Ala	Leu	Ser	Gly	Leu	Pro	His	Phe	Thr	Ala	Met	Ala	Gly	
			340					345					350			
ccg	gag	gat	cta	acg	gga	act	att	ttg	att	gcc	gac	tcg	gta	cgc	cat	1104
Pro	Glu	Asp	Leu	Thr	Gly	Thr	Ile	Leu	Ile	Ala	Asp	Ser	Val	Arg	His	
		355					360					365				
gtc	gag	gaa	gcc	cac	gcc	ctc	att	gcc	ttg	ggg	caa	att	ccc	gat	gct	1152
Val	Glu	Glu	Ala	His	Ala	Leu	Ile	Ala	Leu	Gly	Gln	Ile	Pro	Asp	Ala	
	370					375					380					
aat	ccg	tct	tta	tat	ttg	gat	att	ccc	act	gta	ttg	gac	ccc	acc	atg	1200
Asn	Pro	Ser	Leu	Tyr	Leu	Asp	Ile	Pro	Thr	Val	Leu	Asp	Pro	Thr	Met	
385					390					395					400	
gcc	ccc	cct	ggg	cag	cac	acc	ctc	tgg	atc	gaa	ttt	ttt	gcc	ccc	tac	1248
Ala	Pro	Pro	Gly	Gln	His	Thr	Leu	Trp	Ile	Glu	Phe	Phe	Ala	Pro	Tyr	
			405						410				415			
cgc	atc	gcc	ggg	ttg	gaa	ggg	aca	ggg	tta	atg	ggc	aca	ggg	tgg	acc	1296
Arg	Ile	Ala	Gly	Leu	Glu	Gly	Thr	Gly	Leu	Met	Gly	Thr	Gly	Trp	Thr	
			420				425						430			
gat	gag	tta	aag	gaa	aaa	gtg	gcg	gat	cgg	gtg	att	gat	aaa	tta	acg	1344
Asp	Glu	Leu	Lys	Glu	Lys	Val	Ala	Asp	Arg	Val	Ile	Asp	Lys	Leu	Thr	
		435					440					445				
gac	tat	gcc	cct	aac	cta	aaa	tct	ctg	atc	att	ggg	cgc	cga	gtg	gaa	1392
Asp	Tyr	Ala	Pro	Asn	Leu	Lys	Ser	Leu	Ile	Ile	Gly	Arg	Arg	Val	Glu	

450	455	460	
agt ccc gcc gaa ctg gcc caa cgg ctg gga agt tac aac ggc aat gtc			1440
Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val			
465	470	475	480
tat cat ctg gat atg agt ttg gac caa atg atg ttc ctc cgg cct cta			1488
Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu			
	485	490	495
ccg gaa att gcc aac tac caa acc ccc atc aaa aat ctt tac tta aca			1536
Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr			
	500	505	510
ggg gcg ggt acc cat ccc ggt ggc tcc ata tca ggt atg ccc ggt aga			1584
Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg			
	515	520	525
aat tgc gct cgg gtc ttt tta aaa caa caa cgt cgt ttt tgg taa			1629
Asn Cys Ala Arg Val Phe Leu Lys Gln Gln Arg Arg Phe Trp			
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<212>	PRT		
<213>	Synechocystis sp.		
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Val Cys Ala Ala Tyr Leu Leu Gln Arg Gly Leu Gly Val Thr Leu Leu			
	20	25	30
Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met			
	35	40	45
Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His			
	50	55	60
Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln			
65	70	75	80
Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly			
	85	90	95
Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys			
	100	105	110

Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln
 115 120 125

Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe
 130 135 140

Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp
 145 150 155 160

Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala
 165 170 175

Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn
 180 185 190

Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys
 195 200 205

Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met
 210 215 220

Met Met Val Ala Met Arg His Leu Glu Gly Ile Ala Arg Pro Lys Gly
 225 230 235 240

Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln
 245 250 255

Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu
 260 265 270

Asn Asn Gln Ala Ile Gly Val Glu Val Ala Asn Gly Glu Gln Tyr Arg
 275 280 285

Ala Lys Lys Gly Val Ile Ser Asn Ile Asp Ala Arg Arg Leu Phe Leu
 290 295 300

Gln Leu Val Glu Pro Gly Ala Leu Ala Lys Val Asn Gln Asn Leu Gly
 305 310 315 320

Glu Arg Leu Glu Arg Arg Thr Val Asn Asn Asn Glu Ala Ile Leu Lys
 325 330 335

Ile Asp Cys Ala Leu Ser Gly Leu Pro His Phe Thr Ala Met Ala Gly
 340 345 350

Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His
 355 360 365

Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala
 370 375 380

Asn Pro Ser Leu Tyr Leu Asp Ile Pro Thr Val Leu Asp Pro Thr Met
 385 390 395 400

Ala Pro Pro Gly Gln His Thr Leu Trp Ile Glu Phe Phe Ala Pro Tyr
 405 410 415

Arg Ile Ala Gly Leu Glu Gly Thr Gly Leu Met Gly Thr Gly Trp Thr
 420 425 430

Asp Glu Leu Lys Glu Lys Val Ala Asp Arg Val Ile Asp Lys Leu Thr
 435 440 445

Asp Tyr Ala Pro Asn Leu Lys Ser Leu Ile Ile Gly Arg Arg Val Glu
 450 455 460

Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val
 465 470 475 480

Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu
 485 490 495

Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr
 500 505 510

Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg
 515 520 525

Asn Cys Ala Arg Val Phe Leu Lys Gln Gln Arg Arg Phe Trp
 530 535 540

<210> 23

<211> 776

<212> DNA

<213> Bradyrhizobium sp.

<220>

<221> CDS

<222> (1) .. (774)

<400> 23

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Met His Ala Ala Thr Ala Lys Ala Thr Glu Phe Gly Ala Ser Arg Arg	
1 5 10 15	
gac gat gcg agg cag cgc cgc gtc ggt ctc acg ctg gcc gcg gtc atc	96
Asp Asp Ala Arg Gln Arg Arg Val Gly Leu Thr Leu Ala Ala Val Ile	
20 25 30	
atc gcc gcc tgg ctg gtg ctg cat gtc ggt ctg atg ttc ttc tgg ccg	144
Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro	
35 40 45	
ctg acc ctt cac agc ctg ctg ccg gct ttg cct ctg gtg gtg ctg cag	192
Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln	
50 55 60	
acc tgg ctc tat gta ggc ctg ttc atc atc gcg cat gac tgc atg cac	240
Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His	
65 70 75 80	
ggc tcg ctg gtg ccg ttc aag ccg cag gtc aac cgc cgt atc gga cag	288
Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln	
85 90 95	
ctc tgc ctg ttc ctc tat gcc ggg ttc tcc ttc gac gct ctc aat gtc	336
Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val	
100 105 110	
gag cac cac aag cat cac cgc cat ccc ggc acg gcc gag gat ccc gat	384
Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp	
115 120 125	
ttc gac gag gtg ccg ccg cac ggc ttc tgg cac tgg ttc gcc agc ttt	432
Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe	
130 135 140	
ttc ctg cac tat ttc ggc tgg aag cag gtc gcg atc atc gca gcc gtc	480
Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val	
145 150 155 160	
tcg ctg gtt tat cag ctc gtc ttc gcc gtt ccc ttg cag aac atc ctg	528
Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu	
165 170 175	
ctg ttc tgg gcg ctg ccc ggg ctg ctg tcg gcg ctg cag ctg ttc acc	576
Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr	
180 185 190	
ttc ggc acc tat ctg ccg cac aag ccg gcc acg cag ccc ttc gcc gat	624
Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp	
195 200 205	

cgc cac aac gcg cgg acg agc gaa ttt ccc gcg tgg ctg tcg ctg ctg 672
 Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu
 210 215 220

acc tgc ttc cac ttc ggc ttt cat cac gag cat cat ctg cat ccc gat 720
 Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp
 225 230 235 240

gcg ccg tgg tgg cgg ctg ccg gag atc aag cgg cgg gcc ctg gaa agg 768
 Ala Pro Trp Trp Arg Leu Pro Glu Ile Lys Arg Arg Ala Leu Glu Arg
 245 250 255

cgt gac ta 776
 Arg Asp

<210> 24
 <211> 258
 <212> PRT
 <213> Bradyrhizobium sp.

<400> 24

Met His Ala Ala Thr Ala Lys Ala Thr Glu Phe Gly Ala Ser Arg Arg
 1 5 10 15

Asp Asp Ala Arg Gln Arg Arg Val Gly Leu Thr Leu Ala Ala Val Ile
 20 25 30

Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro
 35 40 45

Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln
 50 55 60

Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His
 65 70 75 80

Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln
 85 90 95

Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val
 100 105 110

Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp
 115 120 125

Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe
 130 135 140

Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val
 145 150 155 160

Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu
 165 170 175

Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr
 180 185 190

Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp
 195 200 205

Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu
 210 215 220

Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp
 225 230 235 240

Ala Pro Trp Trp Arg Leu Pro Glu Ile Lys Arg Arg Ala Leu Glu Arg
 245 250 255

Arg Asp

<210> 25
 <211> 777
 <212> DNA
 <213> Nostoc sp.

<220>
 <221> CDS
 <222> (1)..(777)

<400> 25
 atg gtt cag tgt caa cca tca tct ctg cat tca gaa aaa ctg gtg tta 48
 Met Val Gln Cys Gln Pro Ser Ser Leu His Ser Glu Lys Leu Val Leu
 1 5 10 15
 ttg tca tcg aca atc aga gat gat aaa aat att aat aag ggt ata ttt 96
 Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe
 20 25 30
 att gcc tgc ttt atc tta ttt tta tgg gca att agt tta atc tta tta 144
 Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu

35	40	45	
ctc tca ata gat aca tcc ata att cat aag agc tta tta ggt ata gcc Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala 50 55 60			192
atg ctt tgg cag acc ttc tta tat aca ggt tta ttt att act gct cat Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His 65 70 75 80			240
gat gcc atg cac ggc gta gtt tat ccc aaa aat ccc aga ata aat aat Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn 85 90 95			288
ttt ata ggt aag ctc act cta atc ttg tat gga cta ctc cct tat aaa Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys 100 105 110			336
gat tta ttg aaa aaa cat tgg tta cac cac gga cat cct ggt act gat Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp 115 120 125			384
tta gac cct gat tat tac aat ggt cat ccc caa aac ttc ttt ctt tgg Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp 130 135 140			432
tat cta cat ttt atg aag tct tat tgg cga tgg acg caa att ttc gga Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly 145 150 155 160			480
tta gtg atg att ttt cat gga ctt aaa aat ctg gtg cat ata cca gaa Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu 165 170 175			528
aat aat tta att ata ttt tgg atg ata cct tct att tta agt tca gta Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val 180 185 190			576
caa cta ttt tat ttt ggt aca ttt ttg cct cat aaa aag cta gaa ggt Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly 195 200 205			624
ggg tat act aac ccc cat tgt gcg cgc agt atc cca tta cct ctt ttt Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe 210 215 220			672
tgg tct ttt gtt act tgt tat cac ttc ggc tac cac aag gaa cat cac Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His 225 230 235 240			720
gaa tac cct caa ctt cct tgg tgg aaa tta cct gaa gct cac aaa ata Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile 245 250 255			768
tct tta taa Ser Leu			777

<210> 26
 <211> 258
 <212> PRT
 <213> Nostoc sp.

<400> 26

Met Val Gln Cys Gln Pro Ser Ser Leu His Ser Glu Lys Leu Val Leu
 1 5 10 15

Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe
 20 25 30

Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu
 35 40 45

Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala
 50 55 60

Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 65 70 75 80

Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn
 85 90 95

Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys
 100 105 110

Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp
 115 120 125

Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp
 130 135 140

Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly
 145 150 155 160

Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu
 165 170 175

Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val
 180 185 190

Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly
 195 200 205

Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe
 210 215 220

Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His
 225 230 235 240

Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile
 245 250 255

Ser Leu

<210> 27
 <211> 789
 <212> DNA
 <213> Nostoc punctiforme

<220>
 <221> CDS
 <222> (1)..(789)

<400> 27
 ttg aat ttt tgt gat aaa cca gtt agc tat tat gtt gca ata gag caa 48
 Leu Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln
 1 5 10 15
 tta agt gct aaa gaa gat act gtt tgg ggg ctg gtg att gtc ata gta 96
 Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val
 20 25 30
 att att agt ctt tgg gta gct agt ttg gct ttt tta cta gct att aat 144
 Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn
 35 40 45
 tat gcc aaa gtc cca att tgg ttg ata cct att gca ata gtt tgg caa 192
 Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln
 50 55 60
 atg ttc ctt tat aca ggg cta ttt att act gca cat gat gct atg cat 240
 Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His
 65 70 75 80
 ggg tca gtt tat cgt aaa aat ccc aaa att aat aat ttt atc ggt tca 288
 Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser
 85 90 95
 cta gct gta gcg ctt tac gct gtg ttt cca tat caa cag atg tta aag 336
 Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys

100	105	110	
aat cat tgc tta cat cat cgt cat cct gct agc gaa gtt gac cca gat			384
Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp			
115	120	125	
ttt cat gat ggt aag aga aca aac gct att ttc tgg tat ctc cat ttc			432
Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe			
130	135	140	
atg ata gaa tac tcc agt tgg caa cag tta ata gta cta act atc cta			480
Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu			
145	150	155	160
ttt aat tta gct aaa tac gtt ttg cac atc cat caa ata aat ctc atc			528
Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile			
165	170	175	
tta ttt tgg agt att cct cca att tta agt tcc att caa ctg ttt tat			576
Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr			
180	185	190	
ttc gga aca ttt ttg cct cat cga gaa ccc aag aaa gga tat gtt tat			624
Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr			
195	200	205	
ccc cat tgc agc caa aca ata aaa ttg cca act ttt ttg tca ttt atc			672
Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile			
210	215	220	
gct tgc tac cac ttt ggt tat cat gaa gaa cat cat gag tat ccc cat			720
Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His			
225	230	235	240
gta cct tgg tgg caa ctt cca tct gta tat aag cag aga gta ttc aac			768
Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn			
245	250	255	
aat tca gta acc aat tcg taa			789
Asn Ser Val Thr Asn Ser			
260			

<210> 28
 <211> 262
 <212> PRT
 <213> Nostoc punctiforme

<400> 28

Leu Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln
1 5 10 15

Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val
20 25 30

Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn
35 40 45

Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln
50 55 60

Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His
65 70 75 80

Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser
85 90 95

Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys
100 105 110

Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp
115 120 125

Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe
130 135 140

Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu
145 150 155 160

Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile
165 170 175

Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr
180 185 190

Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr
195 200 205

Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile
210 215 220

Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
225 230 235 240

Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn
245 250 255

Asn Ser Val Thr Asn Ser
260

<210> 29
<211> 762
<212> DNA
<213> Nostoc punctiforme

<220>
<221> CDS
<222> (1)..(762)

<400> 29
gtg atc cag tta gaa caa cca ctc agt cat caa gca aaa ctg act cca 48
Val Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro
1 5 10 15

gta ctg aga agt aaa tct cag ttt aag ggg ctt ttc att gct att gtc 96
Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val
20 25 30

att gtt agc gca tgg gtc att agc ctg agt tta tta ctt tcc ctt gac 144
Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Ser Leu Asp
35 40 45

atc tca aag cta aaa ttt tgg atg tta ttg cct gtt ata cta tgg caa 192
Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln
50 55 60

aca ttt tta tat acg gga tta ttt att aca tct cat gat gcc atg cat 240
Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His
65 70 75 80

ggc gta gta ttt ccc caa aac acc aag att aat cat ttg att gga aca 288
Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr
85 90 95

ttg acc cta tcc ctt tat ggt ctt tta cca tat caa aaa cta ttg aaa 336
Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys
100 105 110

aaa cat tgg tta cac cac cac aat cca gca agc tca ata gac ccg gat 384
Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp
115 120 125

ttt cac aat ggt aaa cac caa agt ttc ttt gct tgg tat ttt cat ttt 432
Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe
130 135 140

atg aaa ggt tac tgg agt tgg ggg caa ata att gcg ttg act att att 480
Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile
145 150 155 160

tat aac ttt gct aaa tac ata ctc cat atc cca agt gat aat cta act 528
Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr

	165		170		175	
tac ttt tgg gtg cta ccc tcg ctt tta agt tca tta caa tta ttc tat						576
Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr						
	180		185		190	
ttt ggt act ttt tta ccc cat agt gaa cca ata ggg ggt tat gtt cag						624
Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln						
	195		200		205	
cct cat tgt gcc caa aca att agc cgt cct att tgg tgg tca ttt atc						672
Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile						
	210		215		220	
acg tgc tat cat ttt ggc tac cac gag gaa cat cac gaa tat cct cat						720
Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His						
	225		230		235	240
att tct tgg tgg cag tta cca gaa att tac aaa gca aaa tag						762
Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys						
	245		250			
<210>	30					
<211>	253					
<212>	PRT					
<213>	Nostoc punctiforme					
<400>	30					
Val Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro						
1	5		10		15	
Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val						
	20		25		30	
Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Leu Ser Leu Asp						
	35		40		45	
Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln						
	50		55		60	
Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His						
65	70		75		80	
Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr						
	85		90		95	
Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys						
	100		105		110	

Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp
 115 120 125

Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe
 130 135 140

Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile
 145 150 155 160

Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr
 165 170 175

Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr
 180 185 190

Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln
 195 200 205

Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile
 210 215 220

Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
 225 230 235 240

Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys
 245 250

<210> 31
 <211> 1608
 <212> DNA
 <213> Haematococcus pluvialis

<220>
 <221> CDS
 <222> (3)..(971)

<400> 31
 ct aca ttt cac aag ccc gtg agc ggt gca agc gct ctg ccc cac atc 47
 Thr Phe His Lys Pro Val Ser Gly Ala Ser Ala Leu Pro His Ile
 1 5 10 15
 ggc cca cct cct cat ctc cat cgg tca ttt gct gct acc acg atg ctg 95
 Gly Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu
 20 25 30
 tcg aag ctg cag tca atc agc gtc aag gcc cgc cgc gtt gaa cta gcc 143

Ser	Lys	Leu	Gln	Ser	Ile	Ser	Val	Lys	Ala	Arg	Arg	Val	Glu	Leu	Ala	
			35					40					45			
cgc	gac	atc	acg	cgg	ccc	aaa	gtc	tgc	ctg	cat	gct	cag	cgg	tgc	tcg	191
Arg	Asp	Ile	Thr	Arg	Pro	Lys	Val	Cys	Leu	His	Ala	Gln	Arg	Cys	Ser	
		50					55					60				
tta	gtt	cgg	ctg	cga	gtg	gca	gca	cca	cag	aca	gag	gag	gcg	ctg	gga	239
Leu	Val	Arg	Leu	Arg	Val	Ala	Ala	Pro	Gln	Thr	Glu	Glu	Ala	Leu	Gly	
	65					70					75					
acc	gtg	cag	gct	gcc	ggc	gcg	ggc	gat	gag	cac	agc	gcc	gat	gta	gca	287
Thr	Val	Gln	Ala	Ala	Gly	Ala	Gly	Asp	Glu	His	Ser	Ala	Asp	Val	Ala	
80					85					90					95	
ctc	cag	cag	ctt	gac	cgg	gct	atc	gca	gag	cgt	cgt	gcc	cgg	cgc	aaa	335
Leu	Gln	Gln	Leu	Asp	Arg	Ala	Ile	Ala	Glu	Arg	Arg	Ala	Arg	Arg	Lys	
				100					105					110		
cgg	gag	cag	ctg	tca	tac	cag	gct	gcc	gcc	att	gca	gca	tca	att	ggc	383
Arg	Glu	Gln	Leu	Ser	Tyr	Gln	Ala	Ala	Ala	Ile	Ala	Ala	Ser	Ile	Gly	
			115					120					125			
gtg	tca	ggc	att	gcc	atc	ttc	gcc	acc	tac	ctg	aga	ttt	gcc	atg	cac	431
Val	Ser	Gly	Ile	Ala	Ile	Phe	Ala	Thr	Tyr	Leu	Arg	Phe	Ala	Met	His	
		130					135					140				
atg	acc	gtg	ggc	ggc	gca	gtg	cca	tgg	ggt	gaa	gtg	gct	ggc	act	ctc	479
Met	Thr	Val	Gly	Gly	Ala	Val	Pro	Trp	Gly	Glu	Val	Ala	Gly	Thr	Leu	
	145					150					155					
ctc	ttg	gtg	gtt	ggt	ggc	gcg	ctc	ggc	atg	gag	atg	tat	gcc	cgc	tat	527
Leu	Leu	Val	Val	Gly	Gly	Ala	Leu	Gly	Met	Glu	Met	Tyr	Ala	Arg	Tyr	
160					165					170					175	
gca	cac	aaa	gcc	atc	tgg	cat	gag	tcg	cct	ctg	ggc	tgg	ctg	ctg	cac	575
Ala	His	Lys	Ala	Ile	Trp	His	Glu	Ser	Pro	Leu	Gly	Trp	Leu	Leu	His	
				180					185					190		
aag	agc	cac	cac	aca	cct	cgc	act	gga	ccc	ttt	gaa	gcc	aac	gac	ttg	623
Lys	Ser	His	His	Thr	Pro	Arg	Thr	Gly	Pro	Phe	Glu	Ala	Asn	Asp	Leu	
			195					200					205			
ttt	gca	atc	atc	aat	gga	ctg	ccc	gcc	atg	ctc	ctg	tgt	acc	ttt	ggc	671
Phe	Ala	Ile	Ile	Asn	Gly	Leu	Pro	Ala	Met	Leu	Leu	Cys	Thr	Phe	Gly	
		210					215					220				
ttc	tgg	ctg	ccc	aac	gtc	ctg	ggg	gcg	gcc	tgc	ttt	gga	gcg	ggg	ctg	719
Phe	Trp	Leu	Pro	Asn	Val	Leu	Gly	Ala	Ala	Cys	Phe	Gly	Ala	Gly	Leu	
	225					230					235					
ggc	atc	acg	cta	tac	ggc	atg	gca	tat	atg	ttt	gta	cac	gat	ggc	ctg	767
Gly	Ile	Thr	Leu	Tyr	Gly	Met	Ala	Tyr	Met	Phe	Val	His	Asp	Gly	Leu	
240					245					250					255	
gtg	cac	agg	cgc	ttt	ccc	acc	ggg	ccc	atc	gct	ggc	ctg	ccc	tac	atg	815
Val	His	Arg	Arg	Phe	Pro	Thr	Gly	Pro	Ile	Ala	Gly	Leu	Pro	Tyr	Met	

260	265	270	
aag cgc ctg aca gtg gcc cac cag cta cac cac agc ggc aag tac ggt			863
Lys Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly			
275	280	285	
ggc gcg ccc tgg ggt atg ttc ttg ggt cca cag gag ctg cag cac att			911
Gly Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile			
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cca ggt gcg gcg gag gag gtg gag cga ctg gtc ctg gaa ctg gac tgg			959
Pro Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp			
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tcc aag cgg tag ggtgcggaac caggcacgct ggtttcacac ctcatgcctg			1011
Ser Lys Arg			
320			
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Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala Arg			
35	40	45	

Asp	Ile	Thr	Arg	Pro	Lys	Val	Cys	Leu	His	Ala	Gln	Arg	Cys	Ser	Leu	50	55	60	
Val	Arg	Leu	Arg	Val	Ala	Ala	Pro	Gln	Thr	Glu	Glu	Ala	Leu	Gly	Thr	65	70	75	80
Val	Gln	Ala	Ala	Gly	Ala	Gly	Asp	Glu	His	Ser	Ala	Asp	Val	Ala	Leu	85	90	95	
Gln	Gln	Leu	Asp	Arg	Ala	Ile	Ala	Glu	Arg	Arg	Ala	Arg	Arg	Lys	Arg	100	105	110	
Glu	Gln	Leu	Ser	Tyr	Gln	Ala	Ala	Ala	Ile	Ala	Ala	Ser	Ile	Gly	Val	115	120	125	
Ser	Gly	Ile	Ala	Ile	Phe	Ala	Thr	Tyr	Leu	Arg	Phe	Ala	Met	His	Met	130	135	140	
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Leu	Val	Val	Gly	Gly	Ala	Leu	Gly	Met	Glu	Met	Tyr	Ala	Arg	Tyr	Ala	165	170	175	
His	Lys	Ala	Ile	Trp	His	Glu	Ser	Pro	Leu	Gly	Trp	Leu	Leu	His	Lys	180	185	190	
Ser	His	His	Thr	Pro	Arg	Thr	Gly	Pro	Phe	Glu	Ala	Asn	Asp	Leu	Phe	195	200	205	
Ala	Ile	Ile	Asn	Gly	Leu	Pro	Ala	Met	Leu	Leu	Cys	Thr	Phe	Gly	Phe	210	215	220	
Trp	Leu	Pro	Asn	Val	Leu	Gly	Ala	Ala	Cys	Phe	Gly	Ala	Gly	Leu	Gly	225	230	235	240
Ile	Thr	Leu	Tyr	Gly	Met	Ala	Tyr	Met	Phe	Val	His	Asp	Gly	Leu	Val	245	250	255	
His	Arg	Arg	Phe	Pro	Thr	Gly	Pro	Ile	Ala	Gly	Leu	Pro	Tyr	Met	Lys	260	265	270	

Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly Gly
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Lys Arg

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atg gaa gtg att gct gca ctg gca cac aaa tac atc atg cac ggc tgg 96
 Met Glu Val Ile Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp
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ggc tgg gga tgg cat ctt tca cat cat gaa ccg cgt aaa ggt gcg ttt 144
 Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
 35 40 45

gaa gtt aac gat ctt tat gcc gtg gtt ttt gct gca tta tcg atc ctg 192
 Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ala Leu Ser Ile Leu
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ctg att tat ctg ggc agt aca gga atg tgg ccg ctc cag tgg att ggc 240
 Leu Ile Tyr Leu Gly Ser Thr Gly Met Trp Pro Leu Gln Trp Ile Gly
 65 70 75 80

gca ggt atg acg gcg tat gga tta ctc tat ttt atg gtg cac gac ggg 288
 Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
 85 90 95

ctg gtg cat caa cgt tgg cca ttc cgc tat att cca cgc aag ggc tac 336
 Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
 100 105 110

ctc aaa cgg ttg tat atg gcg cac cgt atg cat cac gcc gtc agg ggc 384
 Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly

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Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser			
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Lys Leu Gln Ala Thr Leu Arg Glu Arg His Gly Ala Arg Ala Gly Ala			
145	150	155	160
gcc aga gat gcg cag ggc ggg gag gat gag ccc gca tcc ggg aag taa			528
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Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe			
35	40	45	
Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ala Leu Ser Ile Leu			
50	55	60	
Leu Ile Tyr Leu Gly Ser Thr Gly Met Trp Pro Leu Gln Trp Ile Gly			
65	70	75	80
Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly			
85	90	95	
Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr			
100	105	110	
Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly			
115	120	125	
Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser			
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 cagcaggcga aaatcctgtt tgatggtggt tccgaaatcg gcaaaatccc ttataaatca 15660
 aaagaatagc ccgagatagg gttgagtgtt gttccagttt ggaacaagag tccactatta 15720
 aagaacgtgg actccaacgt caaagggcga aaaaccgtct atcagggcga tggcccacta 15780
 cgtgaaccat cacccaaata aagttttttg gggtcgaggt gccgtaaagc actaaatcgg 15840
 aaccctaaag ggagcccccg atttagagct tgacggggaa agccggcgaa cgtggcgaga 15900
 aaggaaggga agaaagcgaa aggagcgggc gccattcagg ctgcgcaact gttggaagg 15960
 gcgatcggtg cgggcctctt cgctattacg ccagctggcg aaagggggat gtgctgcaag 16020
 gcgattaagt tgggtaacgc cagggttttc ccagtcacga cgttgtaaaa cgacggccag 16080
 tgaattcgag ctcggtaccc ggg 16103

<210> 63
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 63
 ggcgtacttg aaggaaccct taccg

25

<210> 64
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 64

attgatgctc ccggtcaccg tgatt

25

<210> 65

<211> 500

<212> DNA

<213> Blakeslea trispora

<400> 65

aatctataca atgctccata gactcacatt gatattgtcg aagatttcga tgctgactta 60

gtagagcaac tacaaaagtt agcagagaag catgatttct taatctttga agaccgcaag 120

tttgcagata tcggtatgtg aattctatct attttttttc tgatgtgtgc atggatgact 180

catgatcata ttcttaggta atactgtcaa gcatcaatat ggcaagggcg ttacaagat 240

tgcttcttgg tctcatatta ctaatgtcga cacagttcct ggagaaggta ttatcaaggg 300

acttgccgaa gtcggcctcc ctcttggtcg tggcttgctt ttgctagcag aaatgtcatc 360

tcaaggtgca ttaactaagg gtatttacac tgccgaatct gtcaatatgg ctgcgcgcaa 420

caaagatttc gtttttggtt ttattgcaca acacaaaatg aatcagtatg atgatgagga 480

ttttgttgct atgtcgctg 500

<210> 66

<211> 611

<212> DNA

<213> Blakeslea trispora

<400> 66

gagattaaaa tagataagga aaagaaagtg aaaagaaatt cggaagcatg gcacattctt 60

ctttttataa atacatgcct gactttcttt ttccatcgat atgatatatg catatgatag 120

atatacaagc aatcttcttc aaggagtttg aaattttgtc ctccaggagc aaaaaaagt 180

ttttttttat acatgtttgt acacaagaat agttaccaat ttgctttggt cttacgtgct 240

gcaagtttat atcgttttca atttctttgt ctttacattt tctttgtcct ttatctttcc 300

tcatttagtc tttgggagaa ttaggaaaag ggagcggaaa ggtaagaaat gcttgcgat 360

tttactaatt cggcaaacat ccaatttggc aaacagcagc ctgtgcaacg ctctcgagat 420

gacagtatct ttgattacac tctaaatctc gatgaccga ccaaaaagag cgaacaaaga 480

aataatcttg tgcattcgaa tatgatggaa gatTTTTTcc cccttattct aaatgttgac 540

atagcgtgta tgttatataa acaaaaagaa attgtacaaa ctttcttttc ttctcttttt 600

attttatctc t 611

<210> 67
 <211> 720
 <212> DNA
 <213> *Blakeslea trispora*

<400> 67
 atgtcaatac tcacttatct ggaatttcat ctctactata cactacctgt ccttgccggca 60
 ttgtgttggc tgctaaagcc gtttcaactca cagcaagaca atctcaagta taaattttta 120
 atgttgatgg ccgcctctac cgcctcgatt tgggacaatt atatcgttta tcatcgcgct 180
 tgggtggtact gtcctacttg tgttgtggct gtcattggct atgtacctct agaagaatac 240
 atgttcttta tcatcatgac tttaatgact gtcgcgttct caaactttgt tatgcgttgg 300
 cacttgcata ctttctttat tagaccaac acttcttggga agcaaact attagtaggc 360
 cttgtgcttg tttcagcttt attggcaatc acttatcatg cttggcactt gacactgcc 420
 aataaacctt cattttatgg ttcattgcac ctttggtatg cttgtcctgt gttggctatt 480
 ctttggtctg gtgctggcga atatatcttg cgtcgacctg tggctgtcct tttgtctatt 540
 gttatcccta gtgtatacct atgttgggct gatatcgctg ctattagtgc tggcacatgg 600
 catatttctc ttagaacaag cactggcaaa atggtagtac ccgatttacc tgtagaagaa 660
 tgctgtttt ttactttgat caacacagtc ttggtttttg ctacctgtgc tatagaccgc 720

<210> 68
 <211> 1089
 <212> DNA
 <213> *Blakeslea trispora*

<400> 68
 ctgtacaaat catctgttca aaatcaaaac cctaaacaag ccatttcctt tttccagcat 60
 gtcaaagagc tagcatgggc cttctgtctt cctgaccaa tgcctcaaca tgaattgttt 120
 gatgatctta ctatcagctg ggatatttta cgtaaagcct caaagtcatt ctatactgca 180
 tctgccgttt ttccaagtta tgtacgtcaa gacttgggtg ttctctatgc tttctgcaga 240
 gctaccgatg acctgtgcga tgatgaatcc aaatctgttc aagaaagaag agaccaatta 300
 gatcttactc gacaatttgt tcgtgatctc tttagccaaa agaccagtgc gcctattgtg 360
 attgattggg aattgtatca aaaccaactt cctgcttctt gtatatcagc ctttagagcc 420
 tttactcgcc ttccgcatgt ccttgaagta gacctgtag aagaactatt agatgggtac 480
 aaatgggatc ttgagcgtcg tcctatcctt gatgaacaag acttggaggc atactctgct 540
 tgtgtggcca gtagtgtggg tgaaatgtgc acacgtgtga ttcttgctca agaccaaag 600

gaaaatgatg cttggataat tgaccgtgca cgtgagatgg ggctgggtgct acaatacgtt 660
 aacattgctc gagacattgt gactgatagc gagactctgg gtcgatgtta tctgcctcaa 720
 caatggctta gaaaagaaga aacagaacaa atacagcaag gcaacgcccg tagcctaggt 780
 gatcaaagac tgttgggctt gtctctgaag cttgtaggaa aggcagacgc tatcatggtg 840
 agagctaaga agggcattga caagttgccg gcaaactgtc aaggcgggtgt acgagctgct 900
 tgccaagtat atgctgcaat tggatctgta ctcaagcagc agaagacaac atatcctaca 960
 agagctcatc taaaaggaag cgaacgtgcc aagattgctc tgttgagtgt atacaacctc 1020
 tatcaatctg aagacaagcc tgtggctctc cgtcaagcta gaaagattaa gagttttttt 1080
 gttgattag 1089

<210> 69
 <211> 611
 <212> DNA
 <213> *Blakeslea trispora*

<400> 69
 agagataaaa taaaagaga agaaaagaaa gtttgtacaa tttctttttg tttatataac 60
 atacacgcta tgtcaacatt tagaataagg gggaaaaaat cttccatcat attcgaatgc 120
 acaagattat ttctttgttc gctctttttg gtcgggtcat cgagatttag agtgtaatca 180
 aagatactgt catctcgaga gcgttgacac ggctgctggt tgccaaattg gatgtttgcc 240
 gaattagtaa aatacgcaag cttttcttac ctttccgctc ctttttcta attctcccaa 300
 agactaaatg aggaaagata aaggacaag aaaatgtaaa gacaaagaaa ttgaaaacga 360
 tataaacttg cagcacgtaa gaccaaagca aattggtaac tattcttgtg taaaaacatg 420
 tataaaaaaa aacttttttt tgctcctgga ggacaaaatt tcaaactcct tgaagaagat 480
 tgcttgata tctatcatat gcatatatca tatcgatgga aaaagaaagt caggcatgta 540
 ttataaaaaa gaagaatgtg ccatgcttcc gaatttcttt tcactttctt ttccttatct 600
 attttaatct c 611

<210> 70
 <211> 882
 <212> DNA
 <213> *Haematococcus pluvialis*

<400> 70
 atgctgtcga agctgcagtc aatcagcgtc aaggcccgcc gcgttgaact agcccgcgac 60
 atcacgcggc ccaaagtctg cctgcatgct cagcgggtgct cgtagttcg gctgcgagtg 120

gcagcaccac agacagagga ggcgctggga accgtgcagg ctgccggcgc gggcgatgag 180
cacagcgccg atgtagcact ccagcagctt gaccgggcta tcgcagagcg tcgtgcccgg 240
cgcaaacggg agcagctgtc ataccaggct gccgccattg cagcatcaat tggcgtgtca 300
ggcattgcc a ttttcgccac ctacctgaga tttgccatgc acatgaccgt gggcggcgca 360
gtgccatggg gtgaagtggc tggcactctc ctcttggtgg ttggtggcgc gctcggcatg 420
gagatgtatg cccgctatgc acacaaagcc atctggcatg agtcgcctct gggctggctg 480
ctgcacaaga gccaccacac acctcgcaact ggaccctttg aagccaacga cttgtttgca 540
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ctggggggcg cctgcttttg agcggggctg ggcacacgc tatacggcat ggcataatg 660
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tacatgaagc gcctgacagt ggcccaccag ctacaccaca gcggcaagta cggtaggcgcg 780
ccctggggta tgttcttggg tccacaggag ctgcagcaca ttccagggtgc ggcggaggag 840
gtggagcgac tggctctgga actggactgg tccaagcggg ag 882

<210> 71
<211> 528
<212> DNA
<213> *Erwinia uredovora*

<400> 71
atgttgtgga tttggaatgc cctgatcggt ttctgtaccg tgattggcat ggaagtgatt 60
gctgcactgg cacacaaata catcatgcac ggctgggggt ggggatggca tctttcacat 120
catgaaccgc gtaaagggtgc gtttgaagtt aacgatcttt atgccgtggt ttttgctgca 180
ttatcgatcc tgctgattta tctgggcagt acaggaatgt ggccgctcca gtggattggc 240
gcaggtatga cggcgtatgg attactctat tttatggtgc acgacgggct ggtgcatcaa 300
cgttggccat tccgctatat tccacgcaag ggctacctca aacggttgta tatggcgcac 360
cgtatgcac acgccgtcag gggcaaagaa ggttgtgttt cttttggctt cctctatgcg 420
ccgcccctgt caaaacttca ggcgacgctc cgggaaagac atggcgctag agcgggcgct 480
gccagagatg cgcagggcgg ggaggatgag cccgcatccg ggaagtaa 528

<210> 72
<211> 762
<212> DNA
<213> *Nostoc sp. PCC73102*

<400> 72
 atgatccagt tagaacaacc actcagtcac caagcaaaac tgactccagt actgagaagt 60
 aaatctcagt ttaaggggct ttccattgct attgtcattg ttagcgcatg ggtcattagc 120
 ctgagtttat tactttccct tgacatctca aagctaaaat tttggatggt attgcctggt 180
 atactatggc aaacatTTTT atatacggga ttatttatta catctcatga tgccatgcat 240
 ggcgtagtat ttccccaaaa caccaagatt aatcatttga ttggaacatt gacctatcc 300
 ctttatgggc ttttaccata tcaaaaacta ttgaaaaaac attgggttaca ccaccacaat 360
 ccagcaagct caatagaccc ggattttcac aatggtaaac accaaagttt ctttgcttgg 420
 tattttcatt ttatgaaagg ttactggagt tgggggcaaa taattgcgtt gactattatt 480
 tataactttg ctaaatacat actccatata ccaagtgata atctaactta cttttgggtg 540
 ctacctcgc ttttaagttc attacaatta ttctattttg gtactttttt accccatagt 600
 gaaccaatag ggggttatgt tcagcctcat tgtgcccaca caattagcgc tcctatttgg 660
 tggtcattta tcacgtgcta tcattttggc taccacgagg aacatcacga atatcctcat 720
 attttcttggg ggcagttacc agaaatttac aaagcaaaat ga 762

<210> 73
 <211> 617
 <212> DNA
 <213> *Haematococcus pluvialis*

<400> 73
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 agcgatgcgt gtgagacggg tatgtcacgg tcgactgggc tgatggccaa tggcatcggc 120
 catgtctggt catcacgggc tgggtgcctg ggtgaagggt atgcacatca tcatgtgcgg 180
 ttggaggggc tggcacagtg tgggctgaac tggagcagtt gtccaggctg gcgttgaatc 240
 agtgaggggt tgtgattggc ggttgtgaag caatgactcc gcccatattc tatttgtggg 300
 agctgagatg atggcatgct tgggatgtgc atggatcatg gtagtgcagc aaactatatt 360
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 ggaggcttga tcgagagagt gggccgtatt ctttgagagg ggaggctcgt gccagaaatg 540
 gtgagtggat gactgtgacg ctgtacattg caggcagggt agatgcactg tctcgattgt 600
 aaaatacatt cagatgc 617

<210> 74
 <211> 1208
 <212> DNA
 <213> *Haematococcus pluvialis*

<400> 74
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 gaagaaacag aacaaataca gcaaggcaac gcccgtagcc taggtgatca aagactgttg 120
 ggcttgtctc tgaagcttgt aggaaaggca gacgctatca tgggtgagagc taagaagggc 180
 attgacaagt tgccggcaaa ctgtcaaggc ggtgtacgag ctgcttgcca agtatatgct 240
 gcaattggat ctgtactcaa gcagcagaag acaacatata ctacaagagc tcatctaaaa 300
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 aagcctgtgg ctctccgtca agctagaaag attaagagtt tttttgttga ttagtgaatt 420
 tttgttttat ttatgtctga tagttcaata aagagacaac acatacaata taaaatcatt 480
 gtctttaaat gttaatttag tagagtgtaa agcctgcatt tttttgtac gcataaacia 540
 tgaattcacc ccgcttctgg tttttaaata attatgtcaa actagggaaa attctttttt 600
 ttctcttcgt tctttttttg gcttgttgtg gagtacacagg cttgtcttca gattgataga 660
 gggtgtatac actcaacaga gcaatcttgg cacgttcgct tcctttttaga tgagctcttg 720
 taggatatgt tgtcttctgc tgcttgagta cagatccaat tgcagcatat acttggcaag 780
 cagctcgtac accgccttga cagtttgccg gcaacttgct aatgcccttc ttagctctca 840
 ccatgatagc gtctgccttt cctacaagct tcagagacaa gcccaacagt ctttgatcac 900
 ctaggctacg ggcgttgctt tgctgtatct gttctgtttc ttcttttcta agccattggt 960
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 tctttaacag aaatttacc ttttgttata agcacatata aaaaaaaga aatttaagat 1080
 gagtaggact tccattctct caaaaatttt attcaatcca taaatgaatt atttttggac 1140
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<210> 75
 <211> 6316
 <212> DNA
 <213> *Blakeslea trispora*

<220>

<221> misc_feature
 <222> (2694)..(2694)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (4263)..(4263)
 <223> n is a, c, g, or t

<400> 75
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 ctatgccaaag atggcaaaaaa ggcaccagaa acccttagtt tattattgca taatccagtc 180
 gagctagtagt ttctgtagct caagcttaac cgaggatctt ggaatcaact cgtctcgtca 240
 ctcttgccga tgatcctaga aatgggtatct atggatgtta tactaacatt gttatctttc 300
 aaggcctcga agatgttatt gttgcgggtga taaataggct gctatgtact gaagttgctc 360
 tgtaaaatga atctagttca ctgcctactc agcaaagtgt tgtttctaata gtctttaaag 420
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 gatggtttat tacaattaga cgctgggaat aagcaaaagg attcatcttt gtaaataaga 540
 gactggtgca tatgaaagca aggatcgtat caaggaatag ttttgatcga gcatcaccag 600
 caaatgctgc taatgttggc ttcttctttg cttcctgaga ttgaatggga tgtgcctaga 660
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<210> 76

<211> 1170

<212> DNA

<213> *Thermus thermophilus*

<400> 76

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<210> 77

<211> 2981

<212> DNA

<213> *Blakeslea trispora*

<400> 77

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taaatgcgaa tatcgttgct gctttgtact tggaaaacgt taggtaaaag ttggttaatg      240
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aagtaacaag caagacaata atagatccaa tggctttcgg tcttacgagt ttgttcagga	360
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<210> 78

<211> 1749

<212> DNA

<213> *Blakeslea trispora*

<400> 78

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<211> 25
<212> DNA
<213> Artificial Sequence

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<220>
<223> Primer

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<400> 79
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<223> Primer

<400> 80
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